WO 2005/030248

SEQUENCE LISTING AP20 RECUENCE LISTING

<110>	BIOAXONE THERAPEUTIQUE	INC.
	MCKERRACHER, LISA	
	LASKO, DANA	

- <120> COMPOSITIONS AND METHODS FOR TREATING TUMOR SPREADING
- <130> 16627-2PCT
- <150> US 10/902,879
- <151> 2004-08-02
- <150> US 60/506,162
- <151> 2003-09-29
- <160> 59
- <170> PatentIn version 3.1
- <210> 1
- <211> 27
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- <223> Oligonucleotide used to remove the stop codon from ADP-ribosyl tr
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gaattettta ggattgatag etgtgee

27

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- <400> 2

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- <223> Sequence of C3APL: includes ADP-ribosyl transferase C3 (Clostrid
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- <220>
- <221> CDS
- <222> (1)..(888)

336

<223>

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Gly	Ser	Ser	Arg	Val	Asp	Leu	Gln	Ala	Cys	Asn	Ala	Tyr	Ser	Ile _.	Asn ·	
1			•	5					10					15		
caa	aag	gct	tat	tca	aat	act	tac	cag	gag	ttt	act	aat	att	gat	caa	96
Gln	Lys	Ala	Tyr	Ser	Asn	Thr	Tyr	Gln	Glu	Phe	Thr	Asn	Ile	Asp	Gln	
			20					25					30			
		•									•					•
qca-	aaa	gct	tgg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga	cta	agc	aaa	144
			Trp				•							•		
	_	35	~	_			40					45				
tca	caa	222	gaa	act	ata	gta	tca	tat	act	aaa	aqc	qct	aqt.	qaa	ata	192
			Glu													
SEI		туъ	Giu	AIA	110		DCI	- y -	4114	- 115	60					
	50					55			•						•	
					·					1			1_ 1_ 1_	4-	.	246
	•		cta													240
Ąsn	Gly	Lys	Leu	Arg	Gln	Asn	Lys	Gly	Val		Asn	GTA	Pne	Pro		
65					70					.75			•	•	80	•
										•						
aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg	288
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	
	•			85					90					95		

aag acc cct gaa aat att atg tta ttt aga ggc gac gac cct gct tat

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr 105 110 100 tta gga aca gaa ttt caa aac act ctt ctt aat tca aat ggt aca att 384 Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile 125 120 115 aat aaa acg gct ttt gaa aag gct aaa gct aag ttt tta aat aaa gat 432 Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp 13.0 140 135 aga ctt gaa tat gga tat att agt act tca tta atg aat gtc tct caa 480 Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln 160 · 150 155 145 ttt gca gga aga cca att att aca caa ttt aaa gta gca aaa ggc tca 528 Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser 175 170 165 aag gca gga tat att gac cct att agt gct ttt cag gga caa ctt gaa 576 Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 180 185 190 atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg 624 Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 205 195 200 tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca 672

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr

210 215 220

gct atc aat cct aaa gaa ttc gtg atg gaa tcc cgc aaa cgc gca agg 720
Ala Ile Asn Pro Lys Glu Phe Val Met Glu Ser Arg Lys Arg Ala Arg
225 230 230 235 240

cag aca tac acc cgg tac cag act cta gag cta gag aag gag ttt cac 768

Gln Thr Tyr Thr Arg Tyr Gln Thr Leu Glu Leu Glu Lys Glu Phe His

245

250

255

ttc aat cgc tac ttg acc cgt cgg cga agg atc gag atc gcc cac gcc

Phe Asn Arg Tyr Leu Thr Arg Arg Arg Arg Ile Glu Ile Ala His Ala

260 265 270

ctg tgc ctc acg gag cgc cag ata aag att tgg ttc cag aat cgg cgc 864
Leu Cys Leu Thr Glu Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg
275 280 285

atg aag tgg aag aag gag aac tga
Met Lys Trp Lys Lys Glu Asn
290 295

<210> 4

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3APLT: includes ADP-ribosyl transferase C3 (Clostrid
ium botulinum) and Antennapedia sequence.

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1 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35
40
45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50' 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met
85 90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu
180 185 190

Met Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr

210 215 220

Ala Ile Asn Pro Lys Glu Phe Val Met Glu Ser Arg Lys Arg Ala Arg
225 230 235 240

Gln Thr Tyr Thr Arg Tyr Gln Thr Leu Glu Leu Glu Lys Glu Phe His

245
250
255

Phe Asn Arg Tyr Leu Thr Arg Arg Arg Ile Glu Ile Ala His Ala 260 265 . 270

Leu Cys Leu Thr Glu Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg
275 280 285

Met Lys Trp Lys Lys Glu Asn
290 295

<210> 5

<211> 774

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3APS: Includes ADP-ribosyl transferase C3 (Clostrid
ium botulinum) and Antennapedia sequence.

<220>

<221> CDS

<222> (1)..(774)

<223>

<400> 5

gga tcc tct aga gtc gac ctg cag gca tgc aat gct tat tcc att aat

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 10 15

caa aag gct tat tca aat act tac cag gag ttt act aat att gat caa 96
Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

gca aaa gct tgg ggt aat gct cag tat aaa aag tat gga cta agc aaa 144
Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys
35 40 45

tca gaa aaa gaa gct ata gta tca tat act aaa agc gct agt gaa ata

192
Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile

50 55 60

aat gga aag cta aga caa aat aag gga gtt atc aat gga ttt cct tca 240
Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

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aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg	28	88
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met		
				85				•	90					95			
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aag	acc	cct	gaa	aat	att	atg	tta	ttt	aga	ggc	gac	gac	cct	gct	tat	33	36
Lys	Thr	Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr		
•			100					105					110		•		
tta	aas	aca	433	+++	caa	220	act	ctt	ctt	aat	tca	aat	aat	aca	att	3 8	34
			_														. .
ьеи	GΤÃ	Thr	GIU	Pne	GTII	ASII		пец	пеп	ASII	DET		GTÅ	TIIL			
		115					120					125					
				•					•			•	·				
aat	aaa	acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat	4:	32
Asn	ГÀ2	Thr	Ala	Phe	Glu	Lys	Ala	Lys	Ala	Lys	Phe	Leu	Asn	Lys	Asp		
	130				•	135					140						
															•		
aga	ctt	gaa	tat	gga	tat	att	agt	act	tca	tta	atg	aat	gtc	tct	caa	48	80
Arg	Leu	Glu	Tyr	Gly.	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	Gln		
145					150					155				·	160		
ttt	gca	gga	aga	cca	att	att	aca	caa	ttt	aaa	gta	gca	aaa	ggc	tca	52	28
Phe	Ala	Gly	Arg	Pro	Ile	Ile	Thr	Gln	Phe	Lys	Val	Ala	Lys	Gly	Ser	•	
				165					170					175			
aad	gca	gga	tat	att	gac	cct	att	agt	act	ttt	cag	gaa	caa	ctt	qaa	5′	76
_	_	Gly														_	-
пуя	wra	GTÅ		TTC	vəħ	FTO	TTC		wra	r IIC		O-Ly			u		
•			180					185					190				

atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu

195 200 205

tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr

210 220

gct atc aat cct aaa gaa ttc cgc cag atc aag att tgg ttc cag aat 720
Ala Ile Asn Pro Lys Glu Phe Arg Gln Ile Lys Ile Trp Phe Gln Asn
225 230 235 240

cgt cgc atg aag tgg aag gtc gac tcg agc ggc cgc atc gtg act 768
Arg Arg Met Lys Trp Lys Lys Val Asp Ser Ser Gly Arg Ile Val Thr

245 250 255

gac tga 774

Asp

<210> · 6

<211> 257

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3APS: Includes ADP-ribosyl transferase C3 (Clostrid
ium botulinum) and Antennapedia sequence.

<400> 6

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35
40
45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met

85

90
95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp 130 135 140

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
145 150 150 160

Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser

165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 180 185 190

Met Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 215 220

Ala Ile Asn Pro Lys Glu Phe Arg Gln Ile Lys Ile Trp Phe Gln Asn 225 230 235 240

Arg Arg Met Lys Trp Lys Lys Val Asp Ser Ser Gly Arg Ile Val Thr

· Asp

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the amplification of Antennapedia sequenc

<400> 7

gaatcccgca aacgcgcaag gcag

24

<210> 8

<211> 27

<212> DNA

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<213> Artificial Sequence
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<223> Oligonucleotide used in the amplification of Antennapedia sequenc
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                                                                    27
tcagttctcc ttcttccact tcatgcg
<210> 9
<211> 54
<212> DNA
<213> Artificial Sequence
<220>
       Oligonucleotide used in the cloning of sequences from Antennapedi
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<400> 9
aattccgcca gatcaagatt tggttccaga atcgtcgcat gaagtggaag aagg
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<210> 10
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<212>
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<213> Artificial Sequence
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15/84

<220>

WO 2005/030248 PCT/CA2004/001763 ·

<223> Oligonucleotide used in the cloning of sequences from Antennapedi
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<400> 10

ggcggtctag ttctaaacca agctcttagc agcgtagttc accttcttcc agct

54

- <210> 11
- <211> 26
- <212> DNA
- <213> Artificial Sequence

<220>

- <223> Oligonucleotide used inthe amplification of a sequence correspond ing to amino acid 27-72 of HIV-1 Tat
- <400> 11

gaatccaagc atccaggaag tcagcc

26

- <210> 12
- <211> 21
- <212> DNA
- <213> Artificial Sequence

<220>

<223> Oligonucleotide used inthe amplification of a sequence correspond
ing to amino acid 27-72 of HIV-1 Tat

<400> 12

accagccacc accttctgat a

21

48

<210> 13

<211> 876

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3-TL: Includes ADP-ribosyl transferase C3 (Clostrid
ium botulinum) and HIV-1 Tat sequence.

<220>

<221> CDS

<222> (1)..(876)

<223>

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Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 5 ` 10 15

caa aag gct tat tca aat act tac cag gag ttt act aat att gat caa 96
Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln

20 25 . 30

gca aaa gct tgg ggt aat gct cag tat aaa aag tat gga cta agc aaa 144

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys. 45 40 35 tca gaa aaa gaa gct ata gta tca tat act aaa agc gct agt gaa ata 192 Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile 60 50 55 aat gga aag cta aga caa aat aag gga gtt atc aat gga ttt cct tca 240 Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser 80 75 65 70 aat tta ata aaa caa gtt gaa ctt tta gat aaa tct ttt aat aaa atg 288 Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met 95 85 90 aag acc cct gaa aat att atg tta ttt aga ggc gac gac cct gct tat 336 Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr 105 110 100 384 tta gga aca gaa ttt caa aac act ctt ctt aat tca aat ggt aca att Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile 125 120 115 aat aaa acg gct ttt gaa aag gct aaa gct aag ttt tta aat aaa gat 432 Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp 130 140 135 · aga ctt gaa tat gga tat att agt act tca tta atg aat gtc tct caa 480 Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln

145					150					155					160	٠
ttt	gca	gga	aga	cca	att	att	aca	caa	ttt	aaa	gta	gca	aaa	ggc	tca	528
Phe	Ala	Gly	Arg	Pro	Ile	Ile	Thr	·Gln	Phe	Lys	Val	Ala	ГЛЗ	Gly	Ser	
•				165					170					175		
aag	gca	gga	tat	att	gac	cct	att	agt	gct	ttt	cag	gga	caa	ctt	gaa	576
Lys	Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Gln	Gly	Gln	Leu	Glu	
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atg	ttg	ctt	cct	aga	cat	agt	act	tat	cat	atạ	gac	gat	atg	aga	ttg	624
Met	Leu	Leu	Pro	Arg	His	Ser	Thr	Tyr	His	Ile	Asp	Asp	Met	Arg	Leu	
		195					200					205		•		
														•		
t.ct	tct	gat	ggt	aaa	caa	ata	ata	att	aca	gca	aca	atg	atg	ggc	aca	672
Ser	Ser	Asp	Gly	Lys	Gln	Ile	Ile	Ile	Thr	Ala	Thr	Met	Met	Gly	Thr	•
	210					215					220					
				•									•			
gct	atc	aat	cct	aaạ	gaa	ttc	aag	cat	cca	gga	agt	cag	cct	aaa	act	72
Ala	Ile	Asn	Pro	Lys	Glu	Phe	Lys	His	Pro	Gly	Ser	Gln	Pro	rys į	Thr	
225					230					235					240	
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gct	tgt	acc	aat	tgc	tat	tgt	aaa	aag	tgt	tgc	ttt	cat	tgc	caa	gtt	.76
Ala	Cys	Thr	Asn	Cys	Tyr	Cys	ГÀЗ	Lys	Cys	Cys	Phe	His	Cys	Gln	Val	
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	Phe													•		
•			260	•		•	-	265			_		270			,

cag cga cga aga gct cat cag aac agt cag act cat caa gct tct cta 864
Gln Arg Arg Arg Ala His Gln Asn Ser Gln Thr His Gln Ala Ser Leu

275 . 280 . 285

tca aag cag taa 876

Ser Lys Gln

290

<210> 14

<211> 291

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3-TL: Includes ADP-ribosyl transferase C3 (Clostrid
ium botulinum) and HIV-1 Tat sequence.

<400> 14

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1 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln

20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35
40
45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met
85 90 95

Lys Thr Pro Glu Asn Île Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100. 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp
130 135 140

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln

145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser 165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu
180 185 190

Met Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 220

Ala Ile Asn Pro Lys Glu Phe Lys His Pro Gly Ser Gln Pro Lys Thr 225 230 235 235 240

Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His Cys Gln Val

Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Arg Arg 260 265 270

Gln Arg Arg Ala His Gln Asn Ser Gln Thr His Gln Ala Ser Leu
275 280 285

Ser Lys Gln

290

<210> 15

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of sequences from HIV-1 Tat

<400> 15

aattctatgg tcgtaaaaaa cgtcgtcaac gtcgtcgtg

39

<210> 16

<211> ,39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of sequences from HIV-1 Tat

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<400> 16
                                                                     39
gataccagca ttttttgcag cagttgcagc agcacagct
<210> 17
<211> 756
<212> DNA
<213> Artificial Sequence
<220>
<223> Sequence of C3-TS: Includes ADP-ribosyl transferase C3 (Clostrid
      ium botulinum) and HIV-1 Tat sequence.
<220>
<221>
      CDS
<222>
      (1)..(756)
<223>
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<400> 17

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Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 10 15

caa aag gct tat tca aat act tac cag gag ttt act aat att gat caa 96

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln

20 25 30

gca	aaa	gct	tgg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga.	cta	agc	aaa	144
Ala	rys.	Ala	Trp	Gly	Asn	Ala	Gln	Tyr	Lys	Lys	Tyr	Gly	Leu	Ser	Lỳs	
		35					40	•				45				
						•										
tca	gaa	aaa	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gct	agt	gaa	ata	192
Ser	Glu	Lys	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ile	
	50					55		·			60					
•																
aat	gga	aag	cta ·	aga	çaa	aat	aag	gga	gtt	atc	aat	gga	ttt	cct	tca	· 240
Asn	Gly	ГЛЗ	Leu	Arg	Gln	Asn	Lys	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser	
65					70					75					80	
							•									
aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg	288
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	
				85					90		•	•		95		
aag	acc	cct	gaa	aat	att	atg	tta	ttt	aga	ggc	gac	gac	cct	gct	tat	330
Lys	Thr	Pŗo	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr	
			100				•	105					110			
											٠					
tta	gga	aca	gaa	ttt	caa	aac	act	ctt	ctt	aat	tca	aat	ggt	aca	att	384
Leu	Gly	Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Asn	Gly	Thr	Ile	•
		115					120					125				
												•				
aat	aaạ	acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat	43
Asn	Lys	Thr	Ala	Phe	Glu	Lys	Ala	ГÀЗ	Ala	Lys	Phe	Leu	Asn	Lys	Asp	
	130		•	•		135					140					
								•			٠	-				
aga	ctt	gaa	tat	qqa	tat	att	agt	act	tca	tta	atg	aat	gtc	tct	caa	48

Arg	Leu	Glu	Tyr	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	Gln	
145					150		-	•		155					160	
ttt	gca	gga	aga	cca	att	att	aca	caa	ttt	aaa	gta	gca	aaa	ggc	tca	528
Phe	Ala	Gly	Arg	Pro	Ile	Ile	Thr	Gln	Phe	Lys	Val	Ala	Lys	Gly	Ser	
				165					170					175		
•																
aag	gca	gga	tat	att	gac	cct	att	agt	gct	ttt	cag	gga	caa	ctt	gaa	· 576
Lys	Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Gln	Gly	Gln	Leu	Glu .	
	•		180				•	185					190			
			•			•										
atg	ttg	ctt	cct	aga	cat	agt	act	tat	cat	ata	gac	gat	atg	aga	ttg	624
Met	Leu	Leu	Pro	Arq	His	Ser	Thr	Tyr	His	Ile	Asp	Asp	Met	Arg	Leu	
		•						_			_	_				
		195				•	200					205				•
		195				,	200					205				
tct	t.ct.		aat.	ааа	caa		,	att	aca	oca	aca		atơ [.]	gac	aca	672
	tct	gat				ata	, ata					atg	_			672
	Ser	gat				ata Ile	, ata				Thr	atg	_			672
		gat				ata	, ata					atg	_			672
Ser	Ser 210	gat Asp	Gly	Lys	Gln	ata Ile 215	ata	Ile	Thr	Ala	Thr 220	atg Met	Met	Gly	Thr	
Ser gct	Ser 210 atc	gat Asp	Gly	Lys	Gln	ata Ile 215	ata Ile	Ile	Thr	Ala	Thr 220 aaa	atg Met	Met	Gly	Thr	720
Ser gct	Ser 210 atc Ile	gat Asp	Gly	Lys	Gln	ata Ile 215	ata Ile	Ile	Thr	Ala	Thr 220 aaa	atg Met	Met	Gly	Thr cgt Arg	
Ser gct	Ser 210 atc Ile	gat Asp	Gly	Lys	Gln	ata Ile 215	ata Ile	Ile	Thr	Ala	Thr 220 aaa	atg Met	Met	Gly	Thr	
Ser gct	Ser 210 atc Ile	gat Asp	Gly	Lys	Gln gaa Glu	ata Ile 215	ata Ile	Ile	Thr	Ala aaa Lys	Thr 220 aaa	atg Met	Met	Gly	Thr cgt Arg	
Ser gct Ala 225	Ser 210 atc Ile	gat Asp aat Asn	Gly cct Pro	Lys aaa Lys	Gln gaa Glu 230	ata Ile 215 ttc	ata Ile tat Tyr	Ile ggt Gly	Thr gct Ala	Ala aaa Lys 235	Thr 220 aaa Lys	atg Met	Met	Gly	Thr cgt Arg	
Ser gct Ala 225	Ser 210 atc Ile	gat Asp aat Asn	Gly cct Pro	Lys aaa Lys tcg	Gln gaa Glu 230	ata Ile 215 ttc Phe	ata Ile tat Tyr	Ile ggt Gly	Thr gct Ala	Ala aaa Lys 235	Thr 220 aaa Lys	atg Met	Met	Gly	Thr cgt Arg	720

<210> 18

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3-TS: Includes ADP-ribosyl transferase C3 (Clostrid ium botulinum) and HIV-1 Tat sequence.

<400> 18

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35
40
45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met
85 90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser 165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu
180 185 190

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 215 220

Ala Ile Asn Pro Lys Glu Phe Tyr Gly Ala Lys Lys Arg Arg Gln Arg 225 230 235 240

Arg Arg Val Asp Ser Ser Gly Pro His Arg Asp
245
250

<210> 19

<211> 1413

<212> DNA

<213> Artificial Sequence

<220>

<223> Includes GST sequences, ADP-ribosyl transferase C3 (C. botulinum
) sequence and a random basic amino acid sequence.

<220>

<221> CDS

<222> (1)..(1413)

<223>

<400> 19 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro 15 10 1 96 act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 20 25 30 tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu 35 45 40 ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys 50 55 tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn 80 65 70 atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 90 85 95 gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt 336

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser

•																
			100					105					110			
						•										
aaa	gac	ttt	gaa	act	ctc	aaa	gtt.	gat	ttt	ctt	agc	aag	cta	cct	gaa	38
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120				•	125				
								•							,	
atg	ctg	aaa	atg	ttc	gaa	gat	cgt	tta	tgt	cat	aaa	aca	tat	tta ·	aat	43
Met	Leu	rys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135			•		140					
ggt	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	gac	gct	ctt	gat	. 48
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Туг	Asp	Ala	Leu	Asp	
145					150					155					160	
			•		•		•									
gtt	gtt	tta	tac	atg	gac	cca	atg	tgc	ctg	gat	gcg	ttc	cca	aaa	tta	. 52
Val	.Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu.	Asp	Ala	Phe	Pro	Lys	Leu	
		•	•	165					170					175		•
								٠				•			•	
			aaa					•								57
Val	Cys	Phe	Lys		Arg	Ile	Glu		Ile	Pro	Gln	Ile		Lys	Tyr	
		•	180					185					190			
				٠									•			
			agc							•						62
Leu	Lys		Ser	Lys	Tyr	Ile			Pro	Leu	GIN			GIN	Ala	
		195					200					205	•			
			-	_	•				. -	1	<u> </u>	مالاست	ـــــــــــــــــــــــــــــــــــــ		~~ -	~ -
acg	ttt	ggt	ggt	ggc	gac	cat	cạt	cca	aaa	rcg	gat	ctg	gtt	ccg	cgt	67

220

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg

215

210

gga	tcc	tct	aga	gtc	gac	ctg	cag	gca	tgc	aat	ġct	tat	tcc	att	aat	720
Gly	Ser	Ser	Arg	Val	Asp	Leu	Gln	Ala	Cys	Asn	Ala	Tyr	Ser	Ile	Asn	
225			•		230					235					240	
						•										
caa	aag	gct	tat	tca	aat	act	tac	cag	gag	ttt	·act	aat	att	gat	caa	768 ·
Gln	Lys	Ala	Tyr	Ser	Asn	Thr	Tyr	Gln	Glu	Phe	Thr	Asn	Ile	Asp	Gln	
				245					250					255		
										•				•		
gca	aaa	gct	tgg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga	cta	agc	aaa	8:16
Ala	Lys	Ala	Trp	Gly	Asn	Ala	Gln	Tyr	Lys	Lys	Tyr	Gly	Leu	Ser	Lys	
			260		• ,	•		265		1			270			
						, .										
tca	gaa	aaa	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gcţ	agt	gaa	ata	864
Ser	Glu	Lys	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ile	
		275	•				280					285				
		÷.														
aat	gga	aag	cta	aga	caa	āat	aag	gga	gtt	atc	aat	gga	ttt	cct	tca	912
Asn	Gly	Lys	Leu	Arg	Gl'n	Asn	ГÀЗ	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser	•
	290	,				295	•				300		•			
						٠		•								•
aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg	960
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	rys	Ser	Phe	Asn	Lys	Met	
305			•		310	•				315					320	
										•						
			gaa													1008
Lys	Thr	Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr	
				325					330					335		

tta	gga	aca	gaa	ttt	caa	aac	act	ctt	ctt	aat	tca	aat	ggt	aca	att	1056
Leu	Gly	Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Àsn	Gly	Thr	Ile	
			340		٠			345					350			
		•						•								
aat	aaa	acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat	1104
Asn	Гуs	Thr	Ala	Phe	Glu	Lys	Ala	ГХЗ	Ala	Lys	Phe	Leu	Asn	Lys	Asp	•
		355					360	•				365		•	•	
			,													
aga	ctt	gaa	tat	gga	tat	att	agt	act	tca	tta	atg	aat	gtt	tct	caa	1152
Arg	Leu	Glu	Tyr	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	·Gln	•
-	370					375			•		380					•
		•				•	,	•					•			
ttt	gca	gga	aga	cca	att	att	aca	aaa	ttt	aaa	gta	gca	aaa	, aac	tca	1200
Phe	Ala	Gly	Arg	Pro	Ile	Ile	Thr	Lys	Phe	Lys	Val	Ala	Гуs	Gly	Ser	
385					390					395					400	
										•						
aag	gca	gga	tat	att	gac	cct	att	agt	gct	ttt	cag	gga	caa	ctt	gaa	1248
Lys	Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Gln	Gly	Gln	Leu	Glu	
				405			•		410		·.			415	•	
																•
atg	ttg	ctt	cct	aga	cat	agt	act	tat	cat	ata	gac	gat	atg	aga	ttg	1296
Met	Leu	Leu	Pro	Arg	His	Ser	Thr	Tyr	His	Ile	Asp	Asp	Met	Arg	Leu	
•			420		•			425					430	•		
															٠	
tct	tct	gat	ggt	aaa	caa	ata	ata	att	aca	gca	aca	atg	atg	ggc	aca	1344
Ser	Ser	Asp	Gly	. Tàs	Gln	Ile	Ile	: Ile	Thr	· Ala	Thr	Met	Met	Gly	Thr	
		435					440	•				445	i		•	
		•												-		
gct	atc	aat	cct	aaa	gaa	ttc	aga	agg	g aaa	caa	aga	aga	aaa	aga	aga	1392

Ala Ile Asn Pro Lys Glu Phe Arg Arg Lys Gln Arg Arg Lys Arg Arg

450 455 460

ctg cag gcg gcc gca tcg tga

1413 .

Leu Gln Ala Ala Ser

465 470

<210> 20

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Includes GST sequences, ADP-ribosyl transferase C3 (C. botulinum
) sequence and a random basic amino acid sequence.

· <400> 20

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro

1 10 15

Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu

35

40

45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser

100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr

180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn 225 230 235 240

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
245
250
255

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

260 265 270

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
275 280 285

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser 290 295 300

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met 305 310 315 320

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

325
330
335

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile

340 345 350

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp
355
360
365

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
370 375 380

Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser

385 390 395 400

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu 405 410 415

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
420 425 430

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr

Ala Ile Asn Pro Lys Glu Phe Arg Arg Lys Gln Arg Arg Lys Arg Arg Arg 450 455 460

Leu Gln Ala Ala Ser 465 470

<210> 21

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Random basic amino acid sequence of C3Basic1

<400> 21

Lys Arg Arg Arg Arg Pro Lys Lys Arg Arg Arg Ala Lys Arg Arg

1 5 10 15

<210> 22

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of a random basic amino acid
sequence in C3Basic1

<400> 22

aagagaaggc gaagaagacc taagaagaga cgaagggcga agaggaga

48

<210> 23

<211> 48

<212> DNA.

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of a random basic amino acid sequence in G3Basic1

<400> 23

ttctcttccg cttcttctgg attcttctct gcttcccgct tctcctct

48

<210> 24

<211> 792

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3Basic1: includes ADP-ribosyl transferase C3 (Clost ridium botulinum) sequence and a sequence encoding a random basic amino acid sequence and a Histidine tag.

<220>

<221> CDS

<222> (1).:(792)

<223>

<400> 24

gga tcc tct aga gtc gac ctg cag gca tgc aat gct tat tcc att aat

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 10 15

caa aag gct tat tca aat act tac cag gag ttt act aat att gat caa 96
Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln

20

25

30

gca	aaa	gct	tgg	ggt .	aat	gct	cag	tat	aaa	aag	tat	gga	cta	agc	aaa	144
Ala	Lys	Ala	Trp	Gly	Asņ	Ala	Gln	Tyr	Lys	Lys	Tyr	Gly	Leu	Ser	Lys	
		35					40					45				
tca	gaa	aaa	gaa	gct	ạta	gta	tca	tat	act	aaa	agc	gct	agt	gaa	ata	192
0-10	a l	T	a]	አ ግ 🕳	τÄΑ		Cox	The roof	™h γ	Taro	Cox.	מות	Ser	Glu	Tla	
ser		пÀв	GIU	Ата	Ile		PCI	TÄT	7.117	пур		wra	DCI	GIU	110	•
	50				•	55					60					
										•			4- 4- 4-		.	
					caa	•										240
Asn	Gly	ГÀЗ	Leu	Arg	Gln	Asn	Lys	Gly	Val	Ile	Asn	GIY	Phe	Pro	Ser	
65					70		•	•		75	٠				80	
aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg	288
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	
•				85					90					95		
		•	•													
aag	acc	cct	gaa	aat	att	atg	tta	ttt	aga	ggc	gac	gac	cct	gct	tat	336
Lys	Thr	Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr	
			100				•	105					110			
																•
tta	gga	aca	gaa	ttt	caa	aac	act	ctt	ctt	aat	tca	aat	ggt	aca	att	384
Leu	Gly	Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Asn	Gly	Thr	Ile	
	~	115		•			120					125				
aat	aaa	acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat	432
Asn	Lys	Thr	Ala	Phe	Glu	Lys	Ala	Lys	Ala	Lys	Phe	Leu	Asn	.FÀ2	Asp	
	130					135					140					

aga	ctt	gaa	tat	gga	tat	att	agt	act	tca	tta	atg	aat	gtt	tct	caa	480
Arg	Leu	Glu	Tyr	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	Gln	
145					150	•				155					160	
ttt	gca	gga	aga	çca	att	att	aca	aaa	ttt	aaa	gta	gca	aaa	ggc	tca	528
Phe	Alá	Gly	Arg	Pro	Ile	Ile	Thr	ГЛЗ	Phe	Lys	Val	Ala	ГЛЗ	Gly	Ser	
				165					170					175		
aag	gca	gga	tat	att	gac	cct	att	agt	gct	ttt	cag	gga	caa	ctt	gaa	576
Lys	Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Gln	Gly	Gln	Leu	Glu	
	•		180					185					190			
atg	ttg	ctt	cct	aga	cat	agt	act	tat	cat	ata	gac	gat	atg	aga	ttg	624
Met	Leu	Leu	Pro	Arg	His	Ser	Thr	Tyr	His	Ile	Asp	Asp	Met	Arg	Leu	
		195					200					205				
					caa				•							672
Ser		-	Gly	Lys	Gln		Ile	Ile	Thr	Ala			Met	GTÀ	rnr	
	210					215			,		220				•	
gct	atc	aat	cct	aaa	gaa	ttc	aag	aga	agg	cga	aga	aga	cct	aag	aag	720
Ala	Ile	Asn	Pro	Lys	Glu	Phe	Lys	Arg	Arg	Arg	Arg	Arg	Pro	Lys	Lys	
225					230					235					240	
					agg											768
Arg	Arg	Arg	Ala	·	Arg	Arg	His	His			His	His	Val		Ser	
				245					250		•			255		

agc ggc cgc atc gtg act gac tga

·792

Ser Gly Arg Ile Val Thr Asp

260

<210> 25

<211> 263

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3Basic1: includes ADP-ribosyl transferase C3 (Clost ridium botulinum) sequence and a sequence encoding a random basic amino acid sequence and a Histidine tag.

<400> 25

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile

PCT/CA2004/001763

50

55

60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met
85 90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp

130 135 140

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln

145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser 165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu
180 185 190

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 215 220

Ala Ile Asn Pro Lys Glu Phe Lys Arg Arg Arg Arg Arg Pro Lys Lys
225 230 230 235 235

Arg Arg Arg Ala Lys Arg Arg His His His His His His Val Asp Ser

Ser Gly Arg Ile Val Thr Asp

260

<210> 26

١,

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Random amino acid sequence of C3Basic2

<400> 26

Lys Arg Arg Arg Lys Lys Arg Arg Gln Arg Arg Arg

1 5 10

<210> 27

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of a random basic amino acid
sequence in C3Basic2

<400> 27

aagcgtcgac gtagaaagaa acgtagacag cgtagacgt

39

<210> 28

<211> 39

<212> DNA

<213> Artificial Sequence

<220> .

<223> Oligonucleotide used in the cloning of a random basic amino acid sequence in C3Basic2

<400> 28

ttcgcagctg catctttctt tgcatctgtc gcatctgca

39

<210> 29

<211> 783

<212> DNA

<213> Artificial Sequence

<220> -

<223> Sequence of C3Basic2: includes sequences from ADP-ribosyl-transf
erase C3 (Clostridium botulinum) and a sequence encoding a random
basic amino acid sequence and a histidine tag.

.<220>

<221> CDS

<222> (1)..(783)

<223>

<400> 29

gga tcc tct aga gtc gac ctg cag gca tgc aat gct tat tcc att aat

48
Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 5 10 15

caa	aag	gct	tat	tca	aat	act	tac	cag	gag	ttt	act	aat	att	gat	caa	96
Gln	Ьуs	Ala	Tyr	Ser	Asn	Thr	Tyr	Gln	Glu	Phe	Thr	Asn	Ile	Asp	Gln	
			20					25		•	٠		30			
gca	aaa	gct	tgg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga	cta	agc	aaa	144
Ala	Lys	Ala	Trp	Gly	Asn	Ala	Gln	Tyr	Lys	Lys	Tyr	Gly	Leu	Ser	ŗÀa	
		35					40	•				45				
tca	gaa	aaa	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gct	ågt	gaa	ata	192
Ser	Glü	Lys	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ile	
	50					55					60					
						•					٠			•		
aat	gga	aag	cta	aga	caa	aat	aag	gga	gtt	atc	aat	gga	ttt	cct	tca	24
Asn	Gly	Lys	Leu	Arg	Gln	Asn	Lys	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser	
65.					70 .					75					80	
													•			
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Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	ГЛЗ	Ser	Phe	Asn	Lys	Met	
				85				·	90					95		. •
aag	acc	cct	gaa	aat	att	atg	tta	ttt	aga	ggc	gac	gac	cct	gct	tat	33
Lys	Thr	Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr	
			100					105		•			110			
						•					•					
tta	gga	aca	gaa	ttt	caa	aac	act	ctt	ctt	aat	tca	aat	ggt	aca	att	38
Leu	Gly	Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Asn	Gly	Thr	Ile	
		115					120					125				٠
		•														•
aat	222	acc	act	+++	· caa	aad	act	222	act	aad	+++	tta	aat	aaa	gát	43

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp aga ctt gaa tat gga tat att agt act tca tta atg aat gtt tct caa Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln ttt gca gga aga cca att att aca aaa ttt aaa gta gca aaa ggc tca Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser aag gca gga tat att gac cct att agt gct ttt cag gga caa ctt gaa Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg Met Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr gct atc aat cct aaa gaa ttc aag cgt cga cgt aga aag aaa cgt aga Ala Ile Asn Pro Lys Glu Phe Lys Arg Arg Arg Arg Lys Lys Arg Arg cag cgt aga cgt cac cac cac cac cac cac gtc gac tcg agc ggc cgc Gln Arg Arg Arg His His His His His Val Asp Ser Ser Gly Arg

245 250 255

atc gtg act gac tga 783

Ile Val Thr Asp

260

<210> 30

<211> 260

<212> PRT

<213> Artificial Sequence

<220>

Sequence of C3Basic2: includes sequences from ADP-ribosyl-transf erase C3 (Clostridium botulinum) and a sequence encoding a random basic amino acid sequence and a histidine tag.

<400> 30

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35 . 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met
.
85 90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp . 130 135 140

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu
180 185 190

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu 195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 220

Ala Ile Asn Pro Lys Glu Phe Lys Arg Arg Arg Arg Lys Lys Arg Arg 235 240

Gln Arg Arg Arg His His His His His Val Asp Ser Ser Gly Arg
245
250
255

Ile Val Thr Asp

260

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<210> 31
<211> 9
<212> PRT
<213> Artificial Sequence .
<220>
<223> Reverse HIV-1 Tat amino acid sequence of C3Basic3
<400> 31
Arg Arg Lys Gln Arg Arg Lys Arg Arg
               5 ·
1
<210> 32
<211> 27
<212>
      DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide used in the cloning of a reverse HIV Tat sequence
      in C3Basic3
<400> 32
                                                                     27
agaaggaaac aaagaagaa aagaaga
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<210> 33

<211> 27

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<212> DNA
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<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of a reverse HIV Tat sequence in C3Basic3

<400> 33

,tcttcctttg tttcttcttt ttcttct

27

<210> 34

<211> 771

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3Basic3: includes sequences from ADP-ribosyl tranfer
 ase C3 (C. botulinum) and a sequence encoding a reverse HIV-1 Tat
 amino acid sequence and a Histidine tag

<220>

<221> CDS

<222> (1)..(771)

<223>

<400> 34

gga tcc tct aga gtc gac ctg cag gca tgc aat gct tat tcc att aat

48

Gly	Ser	Ser	Arg	Val	Asp	Leu	Gln	Ala	Cys	Asn	Ala	Tyr	Ser	Ile	Asn	->
1.				5					10					15		
						•										
caa.	aag	gct	tat	tca	aat	act	tac	cag	gag	ttt	act	aat	att	gat	caa	96
Gln	Lys	Ala	Tyr	Ser	Asn	Thr	Tyr	Gln	Glu	Phe	Thr	Asn	Ile	Asp	Gln	
			20					25					30			1
•				•												
gca	aaa	gct	tgg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga	cta	agc	aaa	144
Ala	Lys	Ala	Trp	Gly	Asn	Ala	Gln	Tyr	Lys	ГÀг	Tyr	Gly	Leu	Ser	Lys	_
		35		•			40					45				·
				•	•										•	
tca	gaa	aaa	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gct	agt	gaa	ata	192
Ser	Glu	Lys	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ile	
	50					55					60	٠				
										•					•	
aat	gga	aag	cta	aga	caa	aat	aag	gga	gtt	atc	aat	gga	ttt	cct	tca	240
Asn	Gly	Lys	Leu	Arg	Gln	Asn	Lys	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser	
65					70					75					80	
									•							
aat	tta	ata	aaa	caa	gtt	gaa	ċtt	tta	gat	aaa	tct	ttt	aat	aaa	atg	288
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	
٠				85					90				•	95		
		•													•	
aag	acc	cct	gaa	aat	att	atg	tta	ttt	aga	ggc	gac	gac	cct	gct	tat	336
Lys	Thr	Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr	•
			100					105					110		•	
tta	gga	aca	gaa	ttt	caa	aac	act	ctt	ctt	aat	tca	aat	ggt	aca	att	384
Leu	Glv	Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Asn	Glv	Thr	Ile	

115 120 125

															•		
aat	t a	ıaa	acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat	432
Ası	n I	ys.	Thr	Ala	Phe	Glu	Lys	Ala	Lys	Ala	Lys	Phe	Leu	Asn	Lys	Asp	
	1	L30					135					140					•
							-										
ag	a c	ctt	gaa	tat	gga	tat	att	agt	act	tca	tta	atg	aat	gtt	tct	caa	480
Ar	g. I	Leu	Glu	Tyr	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	Gln	
14	5					150		•			155			,		160	
															•		,
tt.	t g	gca	gga	aga	cca	att	att	aca	aaa	ttt	aaa	gta	gca	aaa	ggc	tca	. 528
Ph	e ?	Ala	Gly	Arg	Pro	İle	Ile	Thr	Lys	Phe	Lys	Val	Ala	Lys	Gly	Ser	
					165		•			170					175		
aa	g s	gca	gga	tat	att	gac	cct	att	agt	gct	ttt	cag	gga	caa	ctt	gaa	576
Lу	s A	Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Gln	Gly	Gln	Leu	Glu	
				180					185		,		•	190			
at	g t	ttg	ctt	cct	aga	cat	agt	act	tat	cat	ata	gac	gat	atg	aga	ttg	624
Me	t I	Leu	Leu	Pro	Arg	His	Ser	Thr	Tyr	His	Ile	Asp	Asp	Met	Arg	Leu	
			195		•			200					205		•		
																	•
							-			aca							672
Se	r S	Ser	Àsp	Gly	Lys	Gln	Ile	Ile	Ile	Thr	Ala	Thr	Met	Met	Gly	Thr	•
•	4	210					215					220					
			•														•
								_		aaa							720
ΑÌ	a :	Ile	Asn	Pro	_		Phe	Arg	Arg	Lys		Arg	Arg	Lys	Arg		
22	5					230					235					240	

cac cac cac cac cac gtc gac tcg agc ggc cgc atc gtg act gac

His His His His Wal Asp Ser Ser Gly Arg Ile Val Thr Asp

250

255

771

<210> 35

tga

<211> 256

<212> PRT

<213> Artificial Sequence

245

<220>

<223> Sequence of C3Basic3: includes sequences from ADP-ribosyl tranfer
ase C3 (C. botulinum) and a sequence encoding a reverse HIV-1 Tat
amino acid sequence and a Histidine tag

<400> 35

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met
85 90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile

115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp

130 135 140

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser 165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu
180 185 190

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 215 220

Ala Ile Asn Pro Lys Glu Phe Arg Arg Lys Gln Arg Arg Lys Arg Arg 235 240

His His His His His Val Asp Ser Ser Gly Arg Ile Val Thr Asp

245 250 255

<210> 36

<211> 887

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3APLT: includes sequences from ADP-ribosyl transfer ase C3 (Clostridium botulinum) and a sequence encoding a proline rich region.

<220>

<221> CDS

<222> (1)..(747)

<223>

<400> 36

gga tcc tct aga gtc gac ctg cag gca tgc aat gct tat tcc att aat

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 10 15

caa aag gct tat tca aat act tac cag gag ttt act aat att gat caa 96

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln

20 25 30

gca aaa gct tgg ggt aat gct cag tat aaa aag tat gga cta agc aaa 144
Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys .

35 40 45

tca gaa aaa gaa gct ata gta tca tat act aaa agc gct agt gaa ata 192
Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60.

		•		•												•
aat	gga	aag	cta	aga	caa	aat	aag	gga	gtt	atc	aat	gga	ttt	cct	tca	240
Asn	GIy	Lys	Leu	Arg	Gln	Asn	Lys	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser	
65			•		70					75	•				80	
																1.
aat	tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg	288
Asn	Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	
				85					90					95		•
					•											
aag	acc	cct	gaa	aat	att	ato	tta	ttt	aga	aac	gac	qac	cct	act	tat	336
									Arg							
2,5	1111		100					105	3	4 -1	<u>.</u> -	F	110		~ 7 –	
			100					205								
				1 _ 1 _ 1 _				k k	1 4		•					204
			_	•											att .	384
Leu	Gly	Thr	Glu	Phe	Gln	Asn ·	Thr	Leu	Leu	Asn	Ser		Gly	Thr	Ile	
		115					120					125				-
												•	•			
aat	aaa	acg	gct	ttt	gaa	aag	gct	aaa	gct	aag	ttt	tta	aat	aaa	gat	432
Asn	Lys	Thr	Ala	Phe	Glu	ГЛЗ	Ala	Lys	Ala	Lys	Phe	Leu	Asn	Lys	Asp	
	130					135					140					
aga	ctt	gaa	tat	gga	tat	att	agt	act	tca	tta	atg	aat	gtt	tct	caa	480
Arg	Leu	Glu	Tyr	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	Gln	
145					150	•				155					160	
			•													
ttt	qca	qqa	aqa	cca	att	att	aca	aaa	ttt	aaa	gta	gca	aaa	ggc	tca	528
•			•						Phe							•
	- A VA	~-1	3	165				_ ₁ 5	170			6 4	-1-	175	_ ~ ~	
				T02	_				T / U					± / ⊃		

aag	gca	gga	tat	att	gac	cct	att	agt	gct	ttt	gca	gga	caa	ctt	gaa	576
Lys	Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Ala	Gly	Gln	Leu	Glu	
			180		-			185	•				190			•
•										•						
atg	ttg	ctt	cct	aga	cat	agt	act	tat	cat	ata	gac	gat	atg	aga	ttg	624
Met	Leụ	Leu	Pro	Arg	His	Ser	Thr	Tyr	His	Ile	Asp	Asp	Met	Arg	Leu	
		195			معر		200		•			205				
tct	tct	gat	ggt	aaa	caa	ata	ata	att	aca	gca	aca	atg	atg	ggc	aca	672
Ser	Ser	Asp	Gly	Lys	Gln	Ile	Ile	Ile	Thr	Ala	Thr	Met	Met	Gly	Thr	ı
	210					215					220					
									•							
gct	atc	aat	cct	aaa	gaa	ttc	gtg	atg	aat	ccc	gca	aac	gcg	caa	ggc	720
Ala	Ile	Asn	Pro	Lys	Glu	Phe	Val	Met	Asn	Pro	Ala	Asn	Ala	Gln	Gly	
225					230					235					240	•
										•						
aga	cat	aca	ccc	ggt	acc	aga	ctc	tag	agc	taga	gaa	ggag	tttc	ac		767
Arg	His	Thr	Pro	Gly	Thr	Arg	Leu									
				245	ı		,									
											•					
ttc	aatc	gct	actt	gacc	cg t	cggc	gaag	g at	cgag	atcg	ccc	acgo	cct	gtgo	ctcacg	827
gag	cgcc	aga	taaa	gatt	tg g	ttcc	agaa	t cg	lacac	atga	agt	ggaa	igaa	ggag	jaactga	887
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<21	.0>	37								•				•		
<21	.1>	248							•							
<21	.2>	PRT														
J 2 1	2 -	ስ ም ሥ ት ዓ	fici	ם וב	lemie	mce							-			

<220>

<223> Sequence of C3APLT: includes sequences from ADP-ribosyl transfer
ase C3 (Clostridium botulinum) and a sequence encoding a proline
rich region.

<400> 37

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn

1 5 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys

35
40
45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser

70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met

95 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr

100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln

145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser 165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu
180 185 190

Met Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 215 220

Ala Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly
225 230 235 240

Arg His Thr Pro Gly Thr Arg Leu

245

<210> 38

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of C3APLT in pET vector

<400> 38

ggatctggtt ccgcgtcata tgtctagagt'cgacctg

37

. <210> 39

<211> 32

<212> DNA

<213>	Artificial Sequence	
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<400>	39	
cgcgga	tcca ttagttctcc ttcttccact tc	32
<210>	40	
<211>	24	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Oligonucleotide used in the sequencing of C3APLT	
<400>	4 Ò .	•
aaatta	aatac gactcactat aggg	24
<210>	41	
<211>		
<212>		•
<213>	Artificial Sequence	
<220>		
<223>	Oligonucleotide used in the sequencing of C3APLT	

<400> 41

gctagttatt gctcagcgg

1.9

<210> 42

<211> . 888

<212> DNA

<213> Artificial Sequence

<220>

<220>

<221> CDS

<222> (1)...(744)

<223>

<400> 42

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96

48

aag gct tat tca aat act tac cag gag ttt act aat att gat caa gca Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala

20

25

30

aaa	gct	tigg	ggt	aat	gct	cag	tat	aaa	aag	tat	gga	cta	agc	aaa	tca	144
Lys	Ala	Trp	Gly	Asn	Ala	Gln	Tyr	Lys	Lys	Tyr	Gly	Leu	Ser	Lys	Ser	
		35		•		•	40				•	45				,
				•	•			•								
gaa	aaa	gaa	gct	ata	gta	tca	tat	act	aaa	agc	gct	agt	gaa	ata	aat	192
Glu	Lys	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ïle	Asn	
	50					55					60				•	
٠														•	•	
gga	aag	cta	aga	caa	aat	aag	gga	gtt	atc	aat	gga	ttt	cct	tca	aat	240
Gly	Lys	Leu	Arg	Gln	Asn	, ràs	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser	Asn	
65					70					75			•		80	
tta	ata	aaa	caa	gtt	gaa	ctt	tta	gat	aaa	tct	ttt	aat	aaa	atg	aag	288
Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	Lys	
				85	-				90	٠				95		
						•										
									ggc							336
Thr	Pro	Glu			Met	Leu	Phe		Gly ·	Asp	Asp	Pro			Leu	
	•		100					105	•				110		·	,
•			,			_									,	2.2.4
			•						aat -							384
Gly	Thr		Phe	Gln	Asn	Thr			Asn	Ser	Asn		Thr	TTE	Asn	•
		115					120					125				
		•		•	٠					1.1.1.	A. I. a.					420
	-				_			_							aga	432
ьys			hue	GIU	_		_	ATG	Lys			ASN	ъÀг	Asp	wrA	
	130					135					. 140					

Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met 180 185 190 ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg tct Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser 195 200 205 tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca gct Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240	c,tt	gaa	tat	gga	tat	att	agt	act	tca	tta _.	atg	aat	gtt	tct	caa	ttt	480
gca gga aga cca att att aca aaa ttt aaa gta gca aaa ggc tca aag \$22 Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys \$165	Leu	Gľu	Tyr	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	Gln	Phe	•
Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys 165 170 175 gca gga tat att gac cct att agt gct ttt gca gga caa ctt gaa atg Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met 180 185 190 ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg tct Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser 195 200 205 tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca gct Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu	145					150					1:55					160	
Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys 165 170 175 gca gga tat att gac cct att agt gct ttt gca gga caa ctt gaa atg Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met 180 185 190 ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg tct Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser 195 200 205 tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca gct Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu								•							•		•
Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys 165 170 175 gca gga tat att gac cct att agt gct ttt gca gga caa ctt gaa atg Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met 180 185 190 ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg tct Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser 195 200 205 tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca gct Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu						•								•			rán
gea gga tat att gac cet att agt get ttt gea gga caa ett gaa atg 57 Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met 180 185 190 ttg ett eet aga cat agt act tat cat ata gac gat atg aga ttg tet 62 Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser 195 200 205 tet gat ggt aaa caa ata ata att aca gea aca atg atg ggc aca get 67 Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat eet aaa gaa tte gtg atg aat eee gea ace geg caa ggc aga Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca eee ggt ace aga ete tag agetagagaa ggagttteae tteaateget 77 His Thr Pro Gly Thr Arg Leu	_		•	•									•		-		528
gca gga tat att gac cct att agt gct ttt gca gga caa ctt gaa atg 57 Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met 180 185 190 ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg tct 62 Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser 195 200 205 tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca gct Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu	Ala	Gly	Arg	Pro	Ile	Ile	Thr	Lys	Phe	Lys	Val	Ala	Lys	Gly	Ser	Lys	
Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met 180 185 190 ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg tct 62 Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser 195 200 205 tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca gct 67 Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 Cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu					165		•			170	•				175		
Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met 180 185 190 ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg tct 62 Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser 195 200 205 tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca gct 67 Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 Cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu														•			
ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg tct Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser 195 200 205 tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca gct Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga Tle Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct Tris Thr Pro Gly Thr Arg Leu	gca	gga	tat	att	gac	cct	att	agt	gct	ttt	gca	gga	caa	ctt	gaa	atg	576
ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg tct Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser 195 200 205 tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca gct 67 Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 Ris Thr Pro Gly Thr Arg Leu	Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Ala	Gly	Gln	Leu	Glu	Met	
Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser 195 200 205 tot gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca gct Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Tle Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu				180					185					190			
Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser 195 200 205 tot gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca gct Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Tle Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu												•		•			
tot gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca gct 67 Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu	ttg	ctt	cct	aga	cat	agt	act	tat	cat	ata	gac	gat	atg	aga	ttg	tct	624
tet gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca gct Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cet aaa gaa tte gtg atg aat eec gca aac geg caa ggc aga Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca eec ggt ace aga etc tag agetagagaa ggagttteac tteaateget His Thr Pro Gly Thr Arg Leu	Leu	Leu	Pro	Arg	His	Ser	Thr	Tyr	His	Ile	Asp	Asp	Met	Arg	Leu	Ser	
Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu			195				•	200					205				
Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220 atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu															•		
atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225	tct	gat	ggt	aaa	caa	ata	ata	att	aca	gca	aca	atg	atg	ggc	aca	gct	672
atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225	Ser	Asp	Gly	Lys	Gln	Ile	Ile	Ile	Thr	Ala	Thr	Met	Met	Gly	Thr	Ala	
atc aat cct aaa gaa ttc gtg atg aat ccc gca aac gcg caa ggc aga 72 Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu				_											-		
Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu		_	•														
Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg 225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu	atc	aat	.cct	222	caa	ttc	ata	ata	aat	ccc	gca	i aac	aca	caa	aac	aga	720
225 230 235 240 cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu				ı													
cat aca ccc ggt acc aga ctc tag agctagagaa ggagtttcac ttcaatcgct 77 His Thr Pro Gly Thr Arg Leu		ASII	PLO	пуз	GIU			Mec	WOTT	F 1. O			HILU	0111			
His Thr Pro Gly Thr Arg Leu	225					230					233					240	
His Thr Pro Gly Thr Arg Leu			•									•	•				
•	cat	aca	CCC	ggt	acc	aga	ctc	tag	agc	taga	gaa	ggag	tttc	ac t	tcaa	teget	774
245	His	Thr	Pro	Gly	Thr	Arg	Leu				•						
					245		•										

acttgacccg tcggcgaagg atcgagatcg cccacgccct gtgcctcacg gagcgccaga 834

taaagatttg gttccagaat cggcgcatga agtggaagaa ggaggactaa ctga

888

<210> 43

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3APLT in a pET vector: includes sequences from ADP
-ribosyl transferase C3 (Clostridium botulinum) and a sequence en
coding a proline rich region.

<400> 43

Met Ser Arg Val Ala Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn Gln

1 10 15

Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala
20 25 30

Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys Ser

35 40 45

Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn

50 55 60

Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn 65 70 75 80

Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys

85

90

95

Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu
100 105 110

Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn 115 . 120 . 125

Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp Arg

Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe

145 150 155 160

Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys

165 170 175

Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met
180 185 190

Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser

Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala 210 215 220

Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg
225 230 235 240

His Thr Pro Gly Thr Arg Leu

245

<210> 44

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of Antennapedia from C3APL

<400> 44

Val Met Glu Ser Arg Lys Arg Ala Arg Gln Thr Tyr Thr Arg Tyr Gln

1 5 10 15

Thr Leu Glu Leu Glu Lys Glu Phe His Phe Asn Arg Tyr Leu Thr Arg

Arg Arg Ile Glu Ile Ala His Ala Leu Cys Leu Thr Glu Arg Gln
35 40 45

Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys Glu Asn 50 55 60 .

<210> 45

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of Antennapedia from C3APS

<400> 45

Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys

1 10 15

Val Asp Ser

<210> 46

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of HIV-1 Tat from C3-TL

<400> 46

Lys His Pro Gly Ser Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys

1 5 10 15

Lys Lys Cys Cys Phe His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu
20 25 30

Gly Ile Ser Tyr Gly Arg Lys Arg Arg Gln Arg Arg Arg Ala His Gln

35
40
45

Asn Ser Gln Thr His Gln Ala Ser Leu Ser Lys Gln

50 55 60

<210> 47

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of HIV-1 Tat from C3-TS

<400> 47

Tyr Gly Ala Lys Lys Arg Arg Gln Arg Arg Arg Val Asp Ser Ser Gly

1 10 15

Pro His Arg Asp

20

<210> 48

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the proline rich region of C3APLT

<400> 48

Val Met Asn Pro Ala Asn Ala Gln Gly Arg His Thr Pro Gly Thr Arg

1 5 10 15

Leu

<210> 49

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence fused to C3 protein to created C3 Tat-short

<400> 49

Tyr Gly Arg Lys Arg Arg Gln Arg Arg Arg

10

<210> 50

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Reverse sequence of Tat amino acids fused to C3 protein to created C3Basic3

<400> 50

Arg Arg Gln Arg Arg Lys Lys Arg

<210> 51

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> transport peptide rich in Proline

<400> 51

Ala Ala Val Leu Leu Pro Val Leu Leu Ala Ala Pro

1 . 5 . 10

<210> 52

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Sperm fertiline alpha peptide

<400> 52

His Pro Ile Gln Ile Ala Ala Phe Leu Ala Arg Ile Pro Pro Ile Ser

1 5 10 15

Ser Ile Gly Thr Cys Ile Leu Lys

20

<210> 53

<211> '9

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence from the C3Basic3

<400> 53

Arg Arg Lys Gln Arg Arg Lys Arg Arg

1

<210> 54

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<211> 744
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<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3-07Q189A

<400> 54

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<220>

<210> 55

<211> 247

<212> PRT

<213> Artificial Sequence

<223> Amino acid sequence of C3-07Q189A

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<400)> 5	55													
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1				5					10					15	
Lys [°]	Ala	Tyr	Ser	Asn	Thr	Tyr	Gln	Glu	Phe	Thr	Asn	Ile	Asp	Gln	Ala
			20 ·					25					30		
Lys	Ala	Trp	Gly	Asn	Ala	Gln	Tyr	Lys	Lys	Tyr	Gly	Leu	Ser	Lys	Ser
		35					40			•		45			
Glu	Lys	Glu	Ala	Ile	Val	Ser	Tyr	Thr	Lys	Ser	Ala	Ser	Glu	Ile	Asn
	50					55					60				
Gly	Lys	Leu	Arg	Gln	Asn	Lys	Gly	Val	Ile	Asn	Gly	Phe	Pro	Ser	Asn
65					70					75					80
Leu	Ile	Lys	Gln	Val	Glu	Leu	Leu	Asp	Lys	Ser	Phe	Asn	Lys	Met	Lys
				85		•		•	90					95	
Thr	Pro	Glu	Asn	Ile	Met	Leu	Phe	Arg	Gly	Asp	Asp	Pro	Ala	Tyr	Leu
			100					105					110		
Gly	Thr	Glu	Phe	Gln	Asn	Thr	Leu	Leu	Asn	Ser	Asn	Gly	Thr	Ile	Asn
		115					120				•	125	•		
Lys	Thr	Ala	Phe	Glu	Lys	Ala	Lys	Ala	Lys	Phe	Leu	Asn	Lys	Asp	Arg
	130		•	•		135					140				-
Leu	Glu	Tyr	Gly	Tyr	Ile	Ser	Thr	Ser	Leu	Met	Asn	Val	Ser	Gln	Phe
145					150					155			•		160
Ala	Gly	Arg	Pro	Ile	Ile	Thr	Gln	Phe	Lys	Val	Ala	Lys	Gly	Ser	Lys
•				165					170		·			175	٠
Ala	Gly	Tyr	Ile	Asp	Pro	Ile	Ser	Ala	Phe	Gln	Gly	Ala	Leu	Glu	Met
			180					185					190	•	•
Leu	Leu	Pro	Arg	His	Ser	Thr	Tyr	His	Ile	Asp	Asp	Met	Arg	Leu	Ser
		195					200					205			

Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala
210 ' 215 220

Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg
225 230 230 235 240

His Thr Pro Gly Thr Arg Leu

245

<210> 56

<211> 783

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of BA-05

<400> 56

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atgatgggca	cagctatcaa	tcctaaagaa	ttcgtgatga	atcccgcaaa	cgcgcaaggc	720
agacatacac	ccggtaccag	actctagagc	tagagaagga	gtttcacttc	aatcgctact	780
tga		• •				783

<210> 57

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of pET9a-BA-07

<400> 57

Met Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn Gln

1 10 15

Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala
20 25 30

Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys Ser

40
45

Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn
50 55 60

Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn
65 70 75 80

Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys

85

90

95

Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu
.
100 105 110

Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn

115 120 125

Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp Arg

130 135 140

Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe

145 150 155 160

Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys

. 165 170 175

Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met

180 . 185 . 190

Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser

195 . 200 205

Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala

210 · 215 220

Ile Asn Pro Lys Glu Phe Val Met Asn Pro Ala Asn Ala Gln Gly Arg

225 230 235 240

His Thr Pro Gly Thr Arg Leu

245

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<211> 35

<212> DNA

<213> Artificial Sequence

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<223> primer

<400> ·58

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35

<210> 59

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 59

tgcgcgtttg cgggattcat cacgaattct ttagg

35